

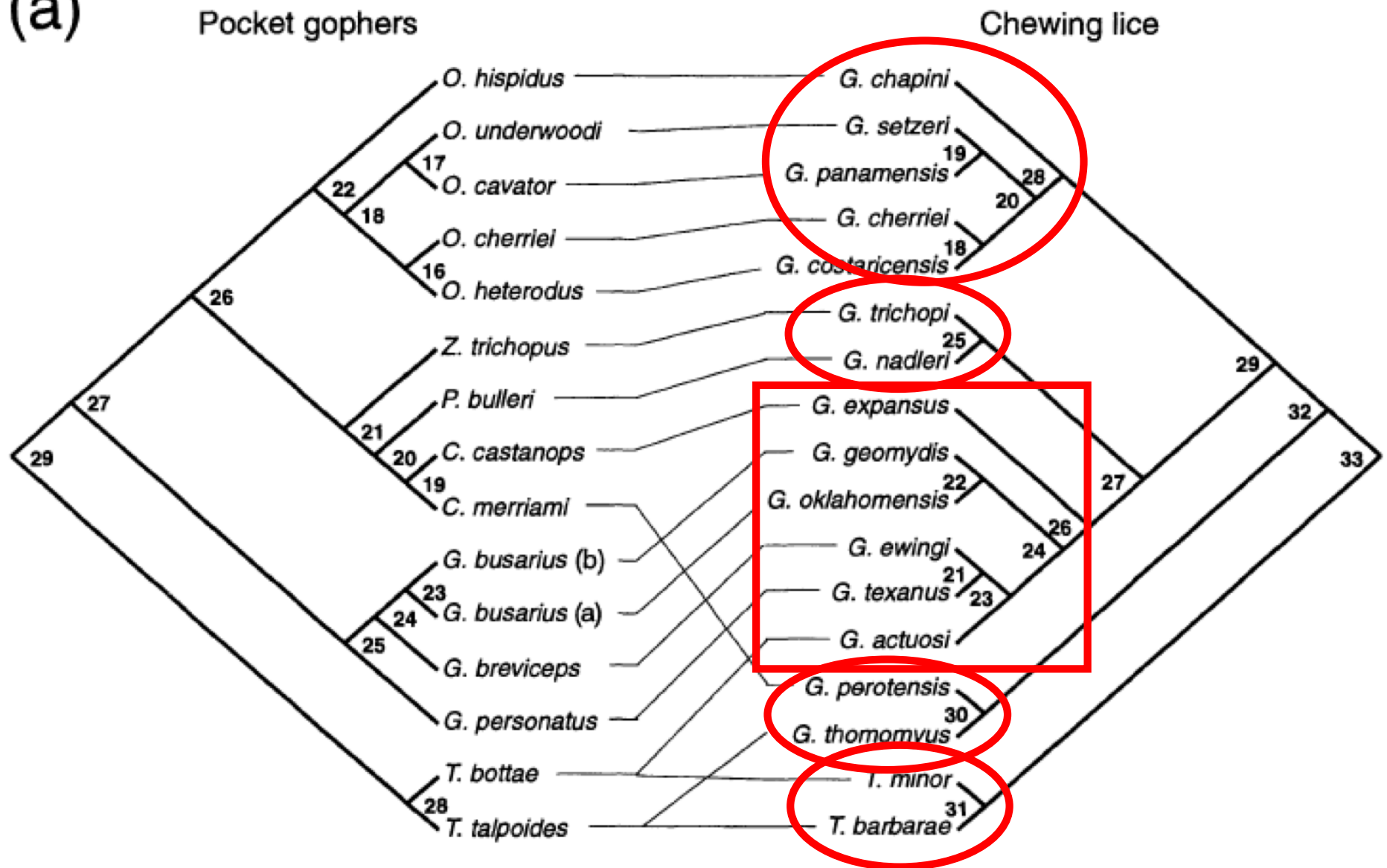
FIGURE 2. A host and parasite phylogeny showing a cospeciation event (●), a duplication (■), a host switch (▶), and a sorting event (○).

3 kinds of speciation events for parasite: cospeciation, host switch, duplication
 sorting: extinction; failure to speciate; 'miss the boat' ; missed collection

Host-parasite evolution vs. Biogeography

- Cospeciation = vicariant speciation event
- Duplication = speciation within region
- Host switch = dispersal to new region + speciation
- Host switch without speciation (expansion of niche breadth) = range expansion to new region without speciation
- Sorting:
 - Vicariance with subsequent extinction in one region
 - Narrowly distributed species that 'miss' vicariant event

(a)



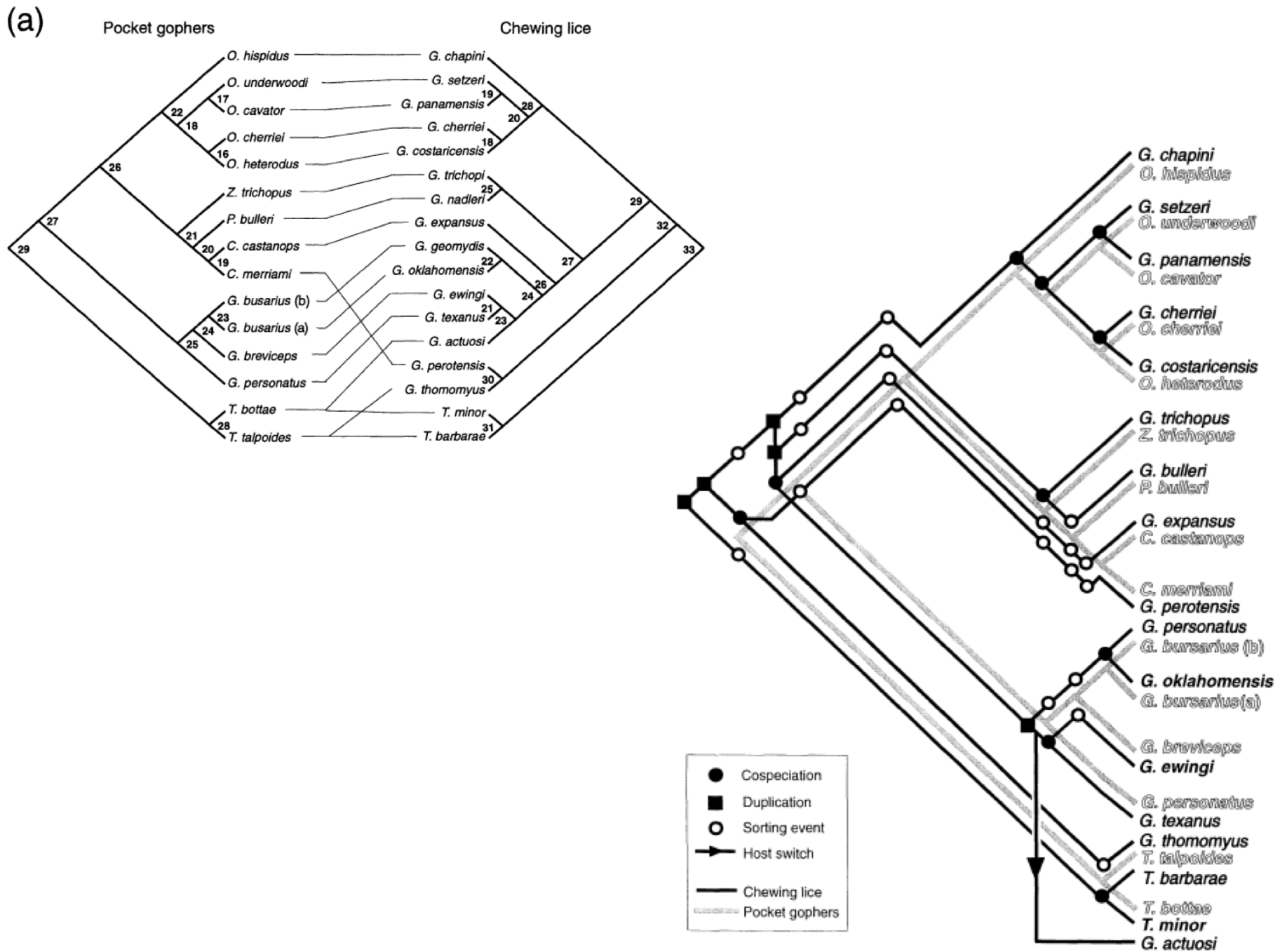


FIGURE 3. A possible reconstruction of the history of the gopher–louse association that postulates 10 cospeciation events, five duplications (in situ speciation of the lice on the same host), 20 sorting events (instances where louse lineages have been lost or remain undetected), and a single host switch (by *Geomydoecus actuosi*).

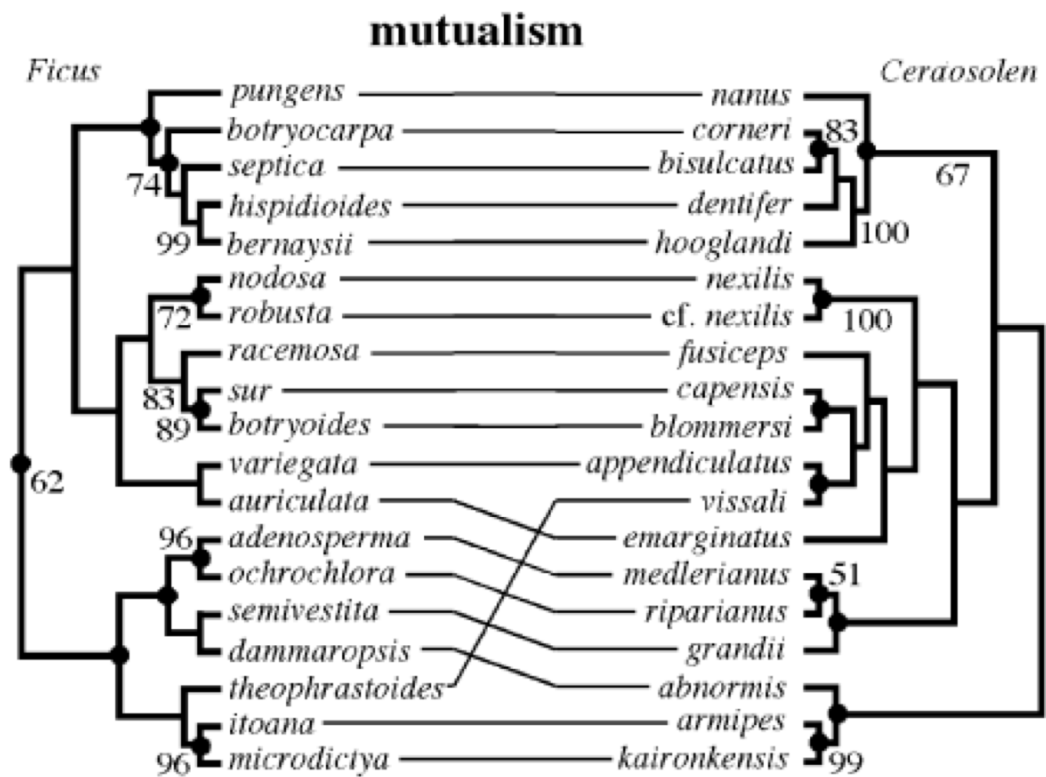
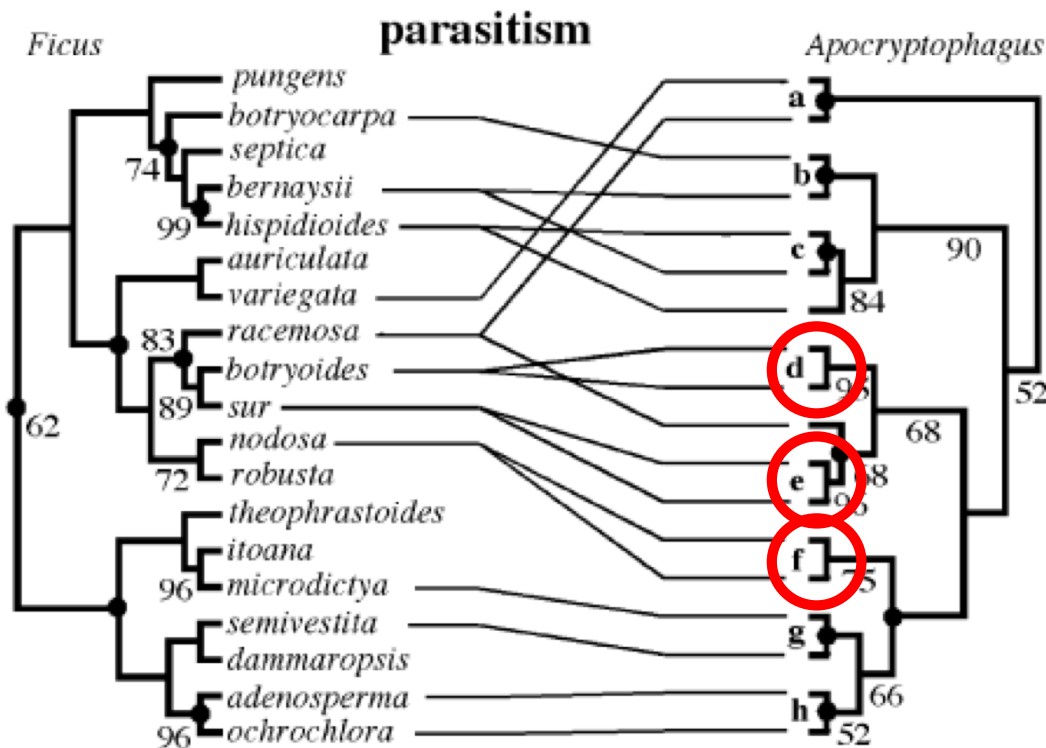


Fig. 2 Evolutionary patterns of host association in pollinating mutualists and nonpollinating parasites of *Ficus* subgenus *Sycomorus sensu lato*. Species associations between pollinating *Ceratosolen* and *Sycomorus* are pairwise, in contrast to *Apocryptophagus*, where multiple unnamed parasite species may attack a single host species and some host species are not attacked at all. Cospeciating nodes inferred from reconciled trees are marked by dots. Bootstrap percentages > 50% based on 1000 replicates are listed below the nodes. Phylogenies are based on parsimony analyses of nuclear ribosomal ITS sequences for *Ficus* and mitochondrial COI sequences for fig wasps. (a–h) refer to species pairs in Fig. 3.



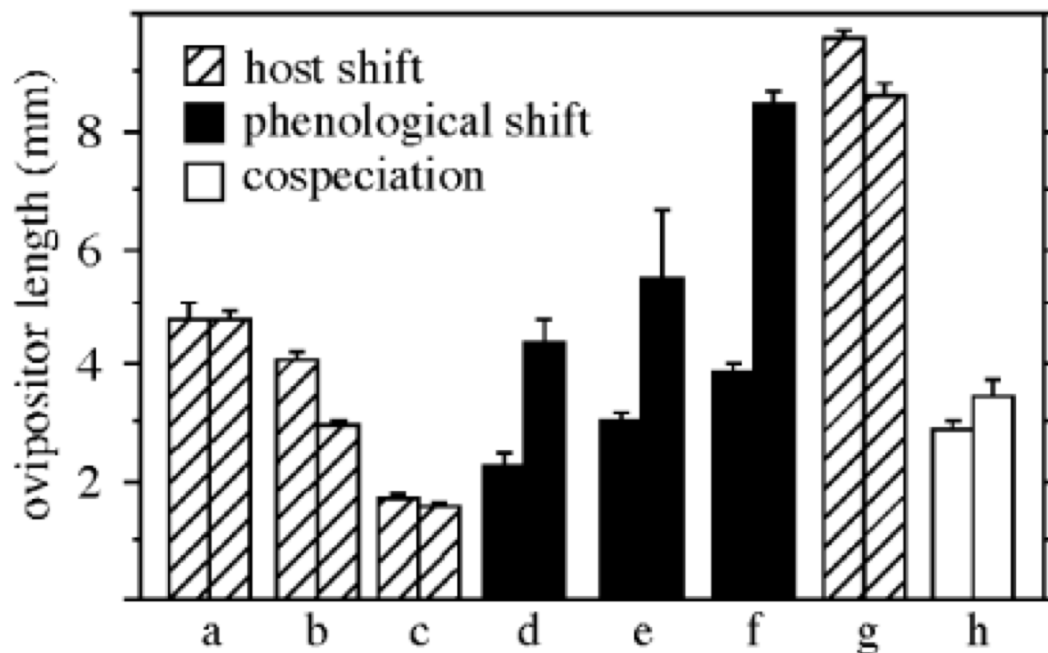


Fig. 3 Sister group comparisons of ovipositor length in the fig parasite, *Apocryptophagus*, under three alternative modes of speciation. (a–h) refer to sister groups in Fig. 2. Sister species (h) attacking sister hosts, *F. adenosperma* and *F. ochrochlora*, represent cospeciation. In contrast (a–c, g) are sister species on nonsister hosts, indicating potential instances of host switching. Closest relatives attacking the same host are represented by (d–f). We predict less divergence in ovipositor length between sister species in cases of cospeciation and host switching than in the case of a phenological shift, where divergence results from a shift in the relative timing of oviposition. Greater ovipositor length divergence between sister species (d–f) indicates a relatively large shift in the timing of oviposition, as the thickness of the fig wall increases during development (Kerdelhue & Rasplus 1996).

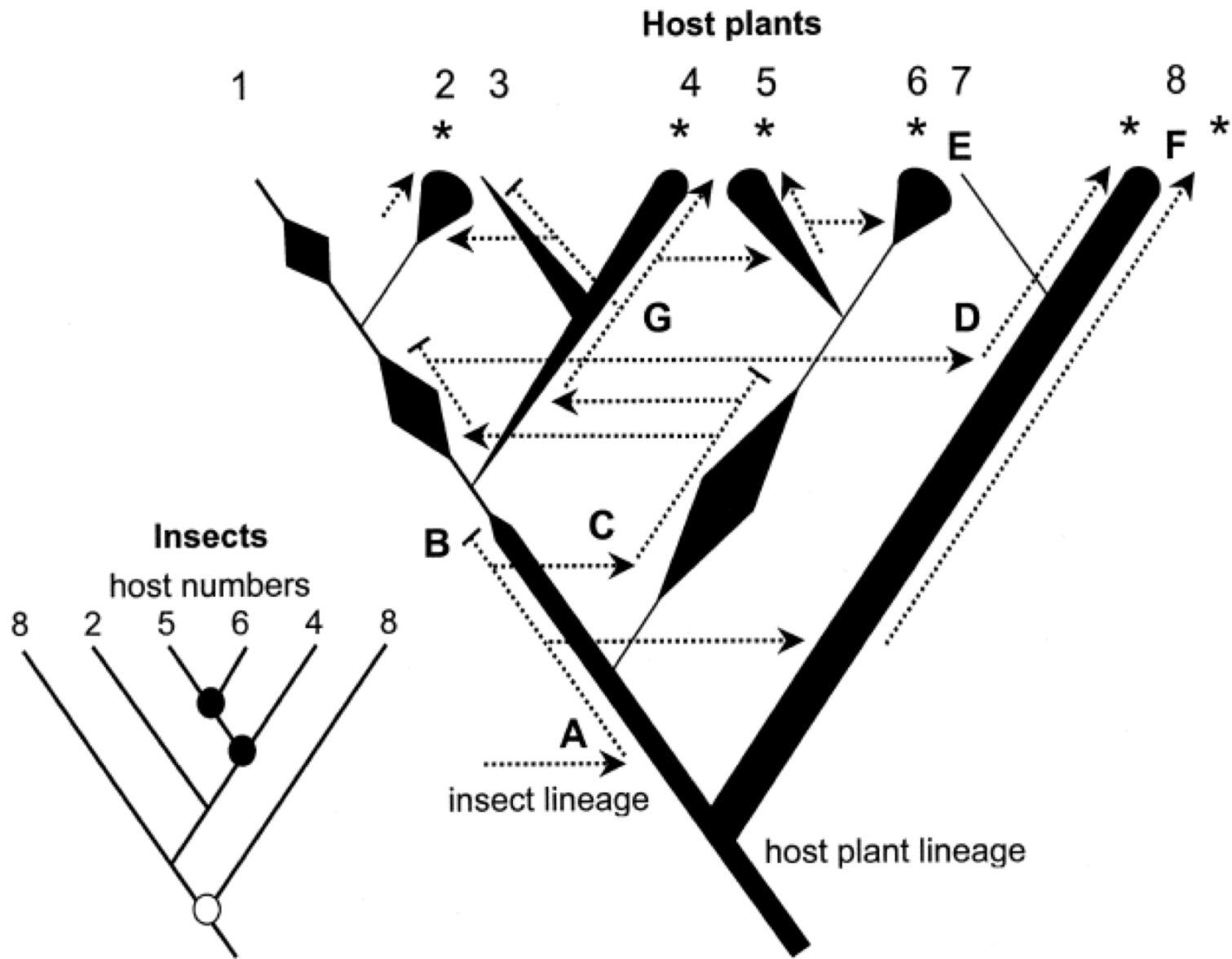
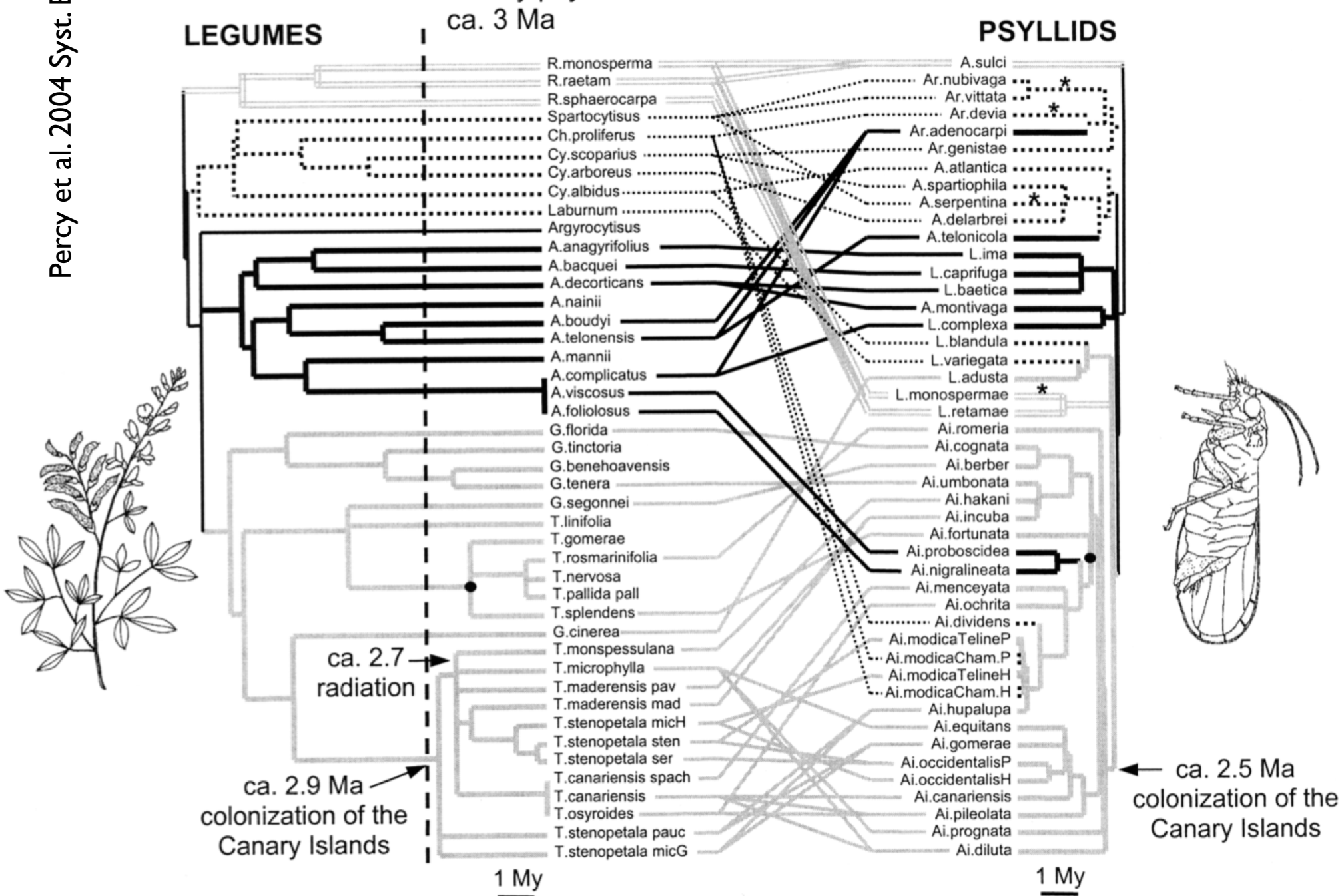


FIGURE 1. A hypothetical fluctuating host plant lineage (right), illustrating the factors that may influence how an insect lineage interacts with a fluctuating plant lineage and an interpretation of the resultant phylogenetic patterns (left). This model takes into account the susceptibility factors for host switching suggested by examination of the ecology of Canary Island psyllids and their legume hosts. Host abundance is indicated by line width. Examples of different events are labeled: A = colonization of preexisting host lineage by insect lineage; B = loss of insect due to extinction; C = increase in host abundance after bottleneck leads to vacant host, usually filled by near host switching from related plants; D = abundant host and geographical proximity may lead to wide host switching; E = rare plants are unlikely to be colonized; F = temporally stable host lineages may sustain multiple insect lineages; G = occasional cospeciation events. The asterisks indicate extant insect taxa, whose phylogeny is shown (left). Given the two phylogenies, certain events would be misinterpreted in a TreeMap analysis: the solid circles are cospeciation events, and the open circle is a duplication event (speciation of parasites in situ on the host).

To get 0 host switches: but assumed 16 cospeciation events (parallel cladogenesis), 29 duplications (parasite speciation without host speciation), and 220 sorting events (parasite loss from host lineage), suggesting that the nonrandom pattern

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colonization of the Genisteae by psyllids:



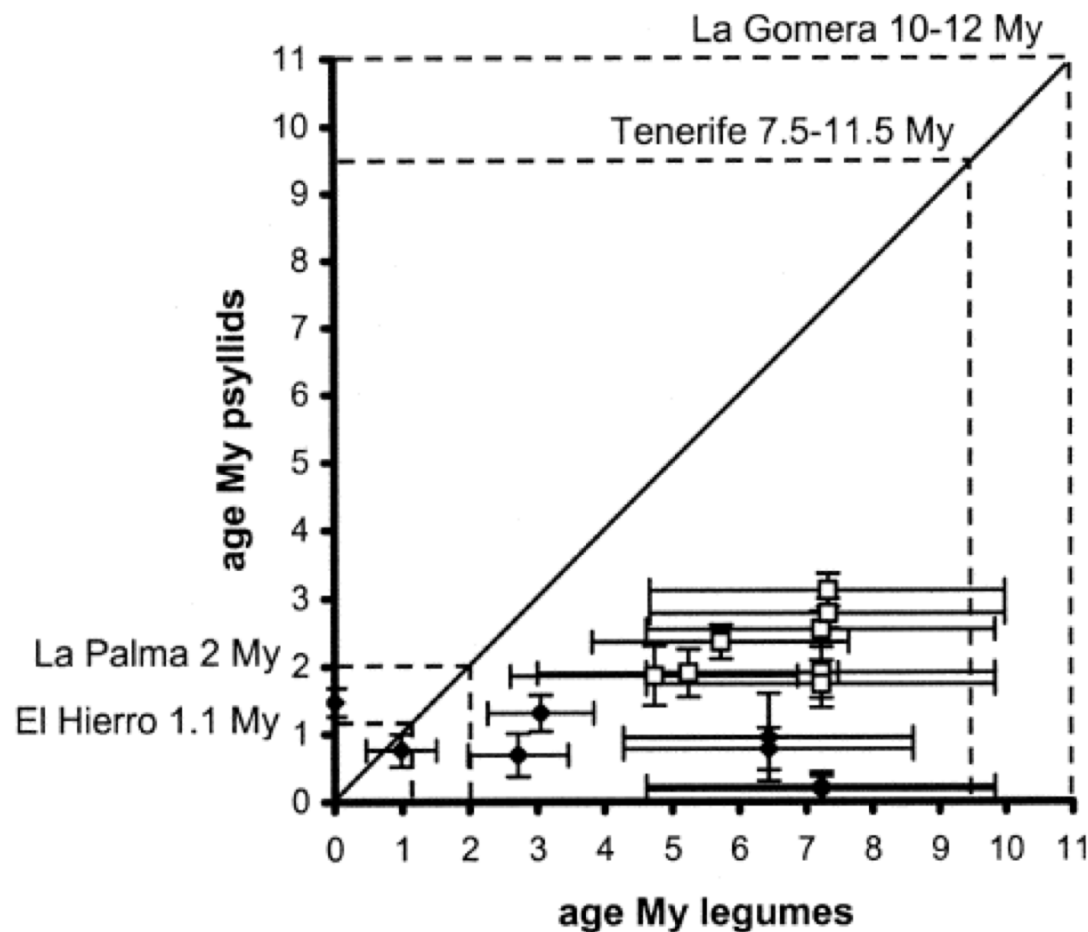
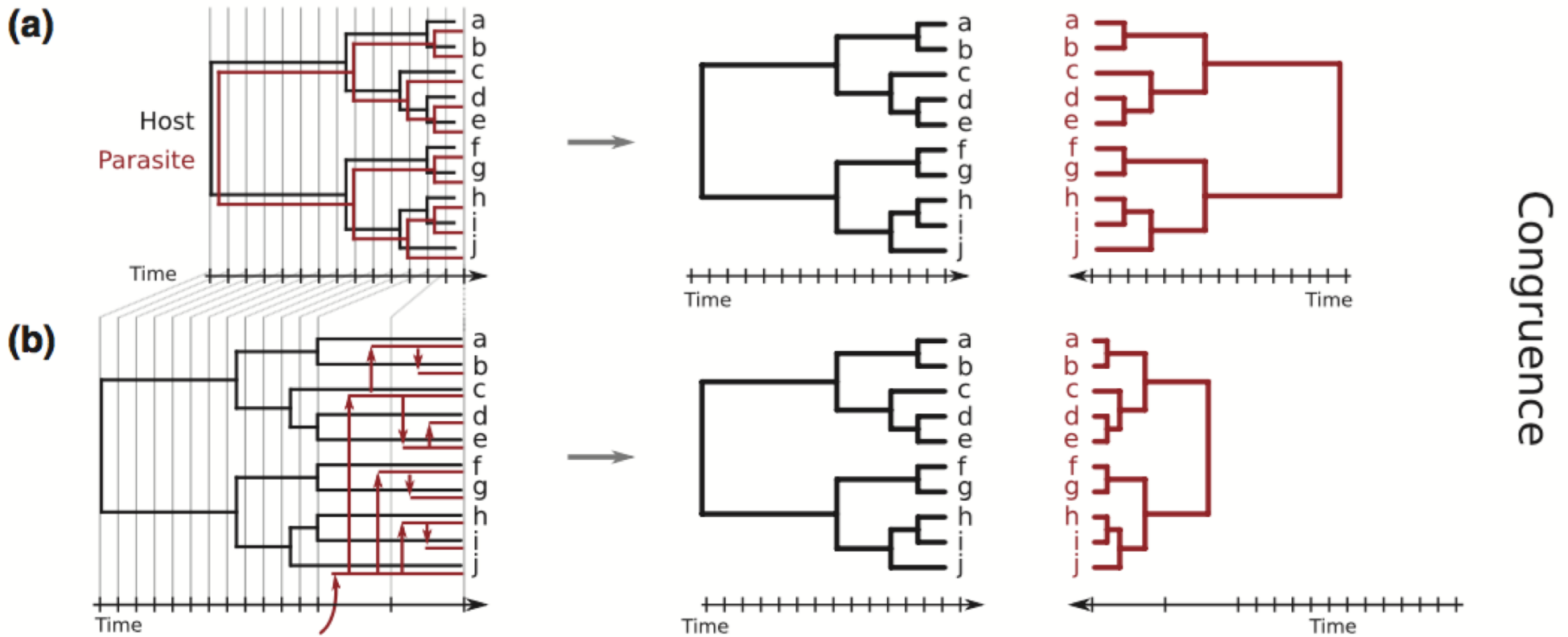
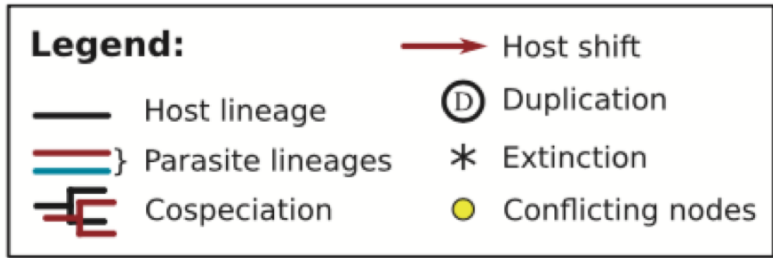
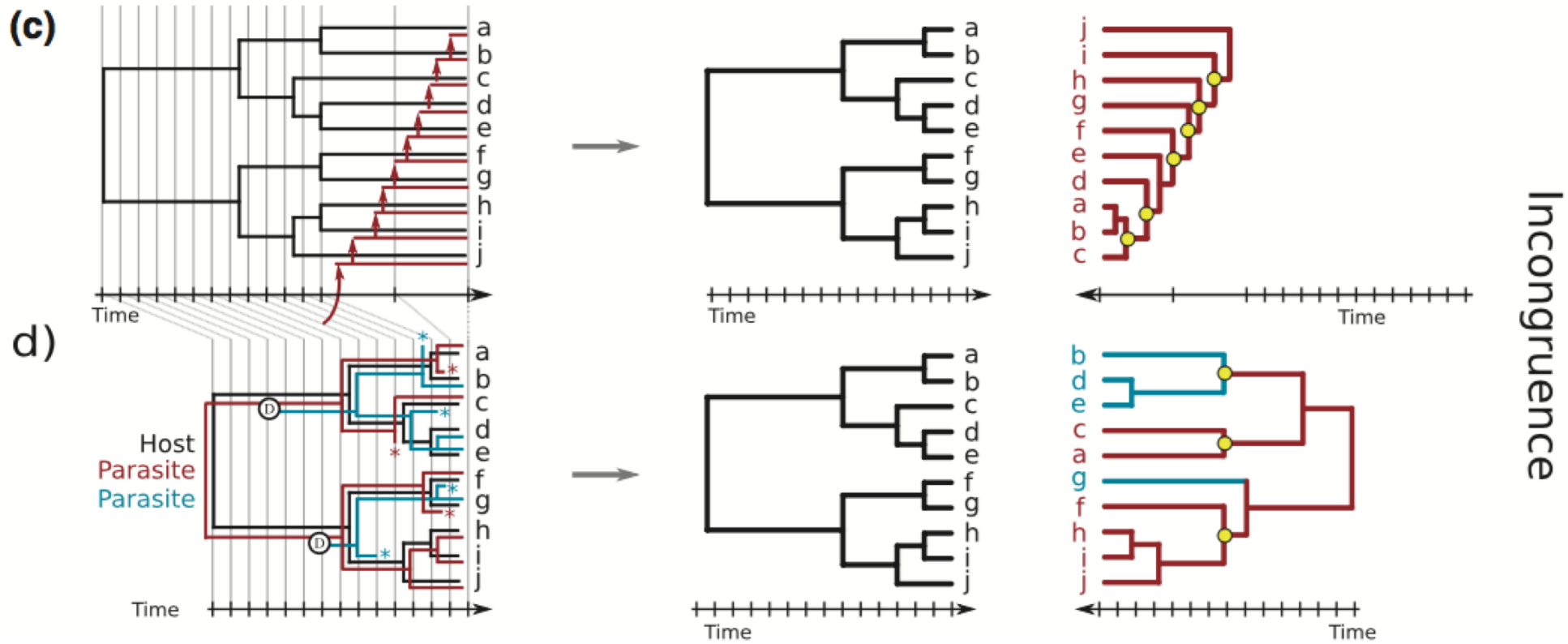


FIGURE 3. Comparative ages of 16 putative cospeciation events suggested by TreeMap (\square = continental; \blacklozenge = island). Reconciled psyllid and legume phylogenies, without considering dates of divergence, produce associated legume nodes that are much older than the putatively synchronous psyllid nodes. This plot shows the cospeciation events determined by TreeMap, which optimizes a psyllid node onto the most recent common ancestor of all its host plants (i.e., no assumption of host switching). All but one of the results are temporally implausible. The dates plotted represent the means and SDs of 100 bootstrap replicates.





5: Unclear cases

(e.g. topological congruence without absolute time inferred or number of other events than cospeciation not provided) ($N = 16$)

1: Convincing cases of cospeciation:

all mutualists ($N = 9$)

3: Significant topological congruence but no concordance of divergence times (either absolute or relative) ($N = 14$)

2: Host shifts likely given the high number of inferred events other than cospeciation ($N = 16$)

4: Host shifts inferred by authors due to lack of phylogenetic congruence ($N = 48$)

